



RAW SEQUENCE LISTING

ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/221,931

Art Unit / Team No. : 01PE

Date Processed by STIC: 1/15/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/221,931

DATE: 01/15/1999
TIME: 12:33:52

Input Set: I221931.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

new format

*Does Not Comply
Corrected Diskette Needed*

use

Unknown - see item 12 on Earm summary sheet

1 <110> APPLICANT: Tsuruo, Takashi
2 Imad, Naasani
3 Seimiya, Hiroyuki
4 Sugano, Haruo
5 <120> TITLE OF INVENTION: Telomerase Inhibitor
6 <130> FILE REFERENCE: WAKAB37.001AUS
7 <140> CURRENT APPLICATION NUMBER: US/09/221,931
8 <141> CURRENT FILING DATE: 1998-12-28
9 <160> NUMBER OF SEQ ID NOS: 6
10 <170> SOFTWARE: FastSEQ for Windows Version 3.0
11 <210> SEQ ID NO 1
12 <211> LENGTH: 18
13 <212> TYPE: DNA
14 <213> ORGANISM: Unknown *Unknown*
15 <400> SEQUENCE: 1
16 aatccgtcga gcagagtt 18
17 <210> SEQ ID NO 2
18 <211> LENGTH: 28
19 <212> TYPE: DNA
20 <213> ORGANISM: Unknown *Unknown*
21 <400> SEQUENCE: 2
22 gtgcccttaa cccttaccct taccctaa 28
23 <210> SEQ ID NO 3
24 <211> LENGTH: 151
25 <212> TYPE: DNA
26 <213> ORGANISM: Unknown
27 <400> SEQUENCE: 3
28 aatcctgtcg agcagagttg tgaatgaggc ctgcgaggct ctgaagagaa gcaccctgct 60
29 caaccccaac cagcggtctgc ctaagggtgga gatcctgcgc agtgccatcc agtacattga 120
30 gcgcctatta gggtaagggt aagggttaagg g 151
31 <210> SEQ ID NO 4
32 <211> LENGTH: 30
33 <212> TYPE: DNA
34 <213> ORGANISM: Unknown
35 <400> SEQUENCE: 4
36 gcgcggctta cccttaccct taccctaacc 30
37 <210> SEQ ID NO 5
38 <211> LENGTH: 36
39 <212> TYPE: DNA
40 <213> ORGANISM: Unknown
41 <400> SEQUENCE: 5
42 aatccgtcga gcagagttaa aaggccgaga agcgat 36
43 <210> SEQ ID NO 6
44 <211> LENGTH: 18

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/221,931DATE: 01/15/1999
TIME: 12:33:52

Input Set: I221931.RAW

45 <212> TYPE: DNA
46 <213> ORGANISM: Unknow
47 <400> SEQUENCE: 6
48 atcgcttctc ggcctttt

18

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VERIFICATION SUMMARY
PATENT APPLICATION US/09/221,931

DATE: 01/15/1999
TIME: 12:33:52

Input Set: I221931.RAW

Line ? Error/Warning

Original Text

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/221,931

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
All text must be visible on page.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and uses spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) features section that some may be missing.
- 7 Wrong Designation Sequence(s) contain amino acid or nucleic acid designators which are not standard
representations as per the Sequence Rules (Please refer to paragraph 1.822)
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
 (1) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of N's or Xaa's Use of N's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 ✓ Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
 (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)
 (Sec. 1.823 of new Sequence Rules)
- 13 Wrong Format File submitted was in the alphabetical heading format of the Old Sequence Rules. This is invalid since the
 "Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Disclosures"
 Federal Register Notice, Vol. 63, No. 104, June 1, 1998, p. 29620
 applies to applications filed on or after July 1, 1998.
 AKS-Biotechnology Systems Branch- 7/10/98



APPLICATION NUMBER	FILING/RECEIPT DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO./TITLE
09/221,931	12/28/98	TSURUO	WAKAB37.001A

020995

0212/0317

NOT ASSIGNED

ENDRE NARTENS OLSON & BEAR LLP
20 NEWPORT CENTER DRIVE
SIXTEENTH FLOOR
NEWPORT BEACH CA 92660

DATE MAILED: 1643

03/17/99

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS
CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application fails to comply with the requirements of 37 CFR 1.821 - 1.825.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. The content of the computer readable form, however, does not comply with the requirements of 37 CFR 1.822 and/or 1.832, as indicated on the attached marked-up copy of the "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).
- ☐ 7. OTHER: _____

APPLICANT MUST PROVIDE:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing."
- ☐ An initial or substitute paper copy of the "Sequence Listing," as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b) or 1.825(d).

FOR QUESTIONS REGARDING COMPLIANCE WITH THESE REQUIREMENTS, PLEASE CONTACT:

- ☐ For Rules Interpretation, call (703) 308-1123.
- ☐ For CRF submission help, call (703) 308-4212.
- ☐ For PatentIn software help, call (703) 308-6856.